

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/732,350DATE: 03/15/2001
TIME: 22:37:44

INPUT SET: S36514.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information

(i) APPLICANT: Svendsen, Allan
Xu, Feng

(ii) TITLE OF THE INVENTION: LACCASE MUTANTS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Novo Nordisk of North America, Inc.
(B) STREET: 405 Lexington Avenue
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10174

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/732,350
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/032,315
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Rozek, Carol
(B) REGISTRATION NUMBER: 36,993
(C) REFERENCE/DOCKET NUMBER: 5200.200-US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-867-0123
(B) TELEFAX: 212-878-9655

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met	Phe	Lys	Asn	Leu	Leu	Ser	Phe	Ala	Leu	Leu	Ala	Ile	Ser	Val	Ala
1				5					10					15	
Asn	Ala	Gln	Ile	Val	Asn	Ser	Val	Asp	Thr	Met	Thr	Leu	Thr	Asn	Ala
				20				25						30	
Asn	Val	Ser	Pro	Asp	Gly	Phe	Thr	Arg	Ala	Gly	Ile	Leu	Val	Asn	Gly
				35				40						45	
Val	His	Gly	Pro	Leu	Ile	Arg	Gly	Gly	Lys	Asn	Asp	Asn	Phe	Glu	Leu
				50				55				60			
Asn	Val	Val	Asn	Asp	Leu	Asp	Asn	Pro	Thr	Met	Leu	Arg	Pro	Thr	Ser
				70						75					80
Ile	His	Trp	His	Gly	Leu	Phe	Gln	Arg	Gly	Thr	Asn	Trp	Ala	Asp	Gly
				85						90					95
Ala	Asp	Gly	Val	Asn	Gln	Cys	Pro	Ile	Ser	Pro	Gly	His	Ala	Phe	Leu
				100						105				110	
Tyr	Lys	Phe	Thr	Pro	Ala	Gly	His	Ala	Gly	Thr	Phe	Trp	Tyr	His	Ser
				115						120				125	
His	Phe	Gly	Thr	Gln	Tyr	Cys	Asp	Gly	Leu	Arg	Gly	Pro	Met	Val	Ile
				130						135				140	
Tyr	Asp	Asp	Asn	Asp	Pro	His	Ala	Ala	Leu	Tyr	Asp	Glu	Asp	Asp	Glu
				150						155					160
Asn	Thr	Ile	Ile	Thr	Leu	Ala	Asp	Trp	Tyr	His	Ile	Pro	Ala	Pro	Ser
				165						170					175
Ile	Gln	Gly	Ala	Ala	Gln	Pro	Asp	Ala	Thr	Leu	Ile	Asn	Gly	Lys	Gly
				180						185				190	
Arg	Tyr	Val	Gly	Gly	Pro	Ala	Ala	Glu	Leu	Ser	Ile	Val	Asn	Val	Glu
				195						200				205	
Gln	Gly	Lys	Lys	Tyr	Arg	Met	Arg	Leu	Ile	Ser	Leu	Ser	Cys	Asp	Pro
				210						215				220	

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100	
101	Asn Trp Gln Phe Ser Ile Asp Gly His Glu Leu Thr Ile Ile Glu Val
102	225 230 235 240
103	
104	Asp Gly Gln Leu Thr Glu Pro His Thr Val Asp Arg Leu Gln Ile Phe
105	245 250 255
106	
107	Thr Gly Gln Arg Tyr Ser Phe Val Leu Asp Ala Asn Gln Pro Val Asp
108	260 265 270
109	
110	Asn Tyr Trp Ile Arg Ala Gln Pro Asn Lys Gly Arg Asn Gly Leu Ala
111	275 280 285
112	
113	Gly Thr Phe Ala Asn Gly Val Asn Ser Ala Ile Leu Arg Tyr Ala Gly
114	290 295 300
115	
116	Ala Ala Asn Ala Asp Pro Thr Thr Ser Ala Asn Pro Asn Pro Ala Gln
117	305 310 315 320
118	
119	Leu Asn Glu Ala Asp Leu His Ala Leu Ile Asp Pro Ala Ala Pro Gly
120	325 330 335
121	
122	Ile Pro Thr Pro Gly Ala Ala Asp Val Asn Leu Arg Phe Gln Leu Gly
123	340 345 350
124	
125	Phe Ser Gly Gly Arg Phe Thr Ile Asn Gly Thr Ala Tyr Glu Ser Pro
126	355 360 365
127	
128	Ser Val Pro Thr Leu Leu Gln Ile Met Ser Gly Ala Gln Ser Ala Asn
129	370 375 380
130	
131	Asp Leu Leu Pro Ala Gly Ser Val Tyr Glu Leu Pro Arg Asn Gln Val
132	385 390 395 400
133	
134	Val Glu Leu Val Val Pro Ala Gly Val Leu Gly Gly Pro His Pro Phe
135	405 410 415
136	
137	His Leu His Gly His Ala Phe Ser Val Val Arg Ser Ala Gly Ser Ser
138	420 425 430
139	
140	Thr Tyr Asn Phe Val Asn Pro Val Lys Arg Asp Val Val Ser Leu Gly
141	435 440 445
142	
143	Val Thr Gly Asp Glu Val Thr Ile Arg Phe Val Thr Asp Asn Pro Gly
144	450 455 460
145	
146	Pro Trp Phe Phe His Cys His Ile Glu Phe His Leu Met Asn Gly Leu
147	465 470 475 480
148	
149	Ala Ile Val Phe Ala Glu Asp Met Ala Asn Thr Val Asp Ala Asn Asn
150	485 490 495
151	
152	Pro Pro Val Glu Trp Ala Gln Leu Cys Glu Ile Tyr Asp Asp Leu Pro

RAW SEQUENCE LISTING PATENT APPLICATION US/09/732,350

 DATE: 03/15/2001
 TIME: 22:37:45

INPUT SET: S36514.raw

	500	505	510
153			
154			
155			
156	Pro Glu Ala Thr Ser Ile Gln Thr Val Val Arg Arg Ala Glu Pro Thr		
157	515	520	525
158			
159	Gly Phe Ser Ala Lys Phe Arg Arg Glu Gly Leu		
160	530	535	
161			
162			
163	(2) INFORMATION FOR SEQ ID NO: 2:		
164			
165	(i) SEQUENCE CHARACTERISTICS:		
166	(A) LENGTH: 499 amino acids		
167	(B) TYPE: amino acid		
168	(C) STRANDEDNESS: single		
169	(D) TOPOLOGY: linear		
170			
171	(ii) MOLECULE TYPE: protein		
172			
173	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:		
174			
175	Gly Ile Gly Pro Val Ala Asp Leu Thr Ile Thr Asn Ala Ala Val Ser		
176	1	5	10 15
177			
178	Pro Asp Gly Phe Ser Arg Gln Ala Val Val Val Asn Gly Gly Thr Pro		
179	20	25	30
180			
181	Gly Pro Leu Ile Thr Gly Asn Met Gly Asp Arg Phe Gln Leu Asn Val		
182	35	40	45
183			
184	Ile Asp Asn Leu Thr Asn His Thr Met Leu Lys Ser Thr Ser Ile His		
185	50	55	60
186			
187	Trp His Gly Phe Phe Gln Lys Gly Thr Asn Trp Ala Asp Gly Pro Ala		
188	65	70	75 80
189			
190	Phe Ile Asn Gln Cys Pro Ile Ser Ser Gly His Ser Phe Leu Tyr Asp		
191	85	90	95
192			
193	Phe Gln Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu		
194	100	105	110
195			
196	Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp		
197	115	120	125
198			
199	Pro Asn Asp Pro Ala Ala Asp Leu Tyr Asp Val Asp Asn Asp Asp Thr		
200	130	135	140
201			
202	Val Ile Thr Leu Val Asp Trp Tyr His Val Ala Ala Lys Leu Gly Pro		
203	145	150	155 160
204			
205	Ala Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Lys Gly Arg		

	165							170							175		
206																	
207																	
208	Ser	Pro	Ser	Thr	Thr	Thr	Ala	Asp	Leu	Ser	Val	Ile	Ser	Val	Thr	Pro	
209				180					185					190			
210																	
211	Gly	Lys	Arg	Tyr	Arg	Phe	Arg	Leu	Val	Ser	Leu	Ser	Cys	Asp	Pro	Asn	
212			195					200					205				
213																	
214	Tyr	Thr	Phe	Ser	Ile	Asp	Gly	His	Asn	Met	Thr	Ile	Ile	Glu	Thr	Asp	
215		210					215					220					
216																	
217	Ser	Ile	Asn	Thr	Ala	Pro	Leu	Val	Val	Asp	Ser	Ile	Gln	Ile	Phe	Ala	
218	225					230					235					240	
219																	
220	Ala	Gln	Arg	Tyr	Ser	Phe	Val	Leu	Glu	Ala	Asn	Gln	Ala	Val	Asp	Asn	
221					245						250				255		
222																	
223	Tyr	Trp	Ile	Arg	Ala	Asn	Pro	Asn	Phe	Gly	Asn	Val	Gly	Phe	Thr	Gly	
224				260						265				270			
225																	
226	Gly	Ile	Asn	Ser	Ala	Ile	Leu	Arg	Tyr	Asp	Gly	Ala	Ala	Ala	Val	Glu	
227			275					280					285				
228																	
229	Pro	Thr	Thr	Thr	Gln	Thr	Thr	Ser	Thr	Ala	Pro	Leu	Asn	Glu	Val	Asn	
230		290					295					300					
231																	
232	Leu	His	Pro	Leu	Val	Thr	Thr	Ala	Val	Pro	Gly	Ser	Pro	Val	Ala	Gly	
233	305					310					315					320	
234																	
235	Gly	Val	Asp	Leu	Ala	Ile	Asn	Met	Ala	Phe	Asn	Phe	Asn	Gly	Thr	Asn	
236					325					330					335		
237																	
238	Phe	Phe	Ile	Asn	Gly	Ala	Ser	Phe	Thr	Pro	Pro	Thr	Val	Pro	Val	Leu	
239				340					345					350			
240																	
241	Leu	Gln	Ile	Ile	Ser	Gly	Ala	Gln	Asn	Ala	Gln	Asp	Leu	Leu	Pro	Ser	
242			355					360					365				
243																	
244	Gly	Ser	Val	Tyr	Ser	Leu	Pro	Ser	Asn	Ala	Asp	Ile	Glu	Ile	Ser	Phe	
245		370					375					380					
246																	
247	Pro	Ala	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Pro	His	Pro	Phe	His	Leu	His	
248	385					390					395						

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text